

RAW SEQUENCE LISTING

DATE: 04/18/2001

PATENT APPLICATION: US/09/218,913B

TIME: 10:40:11

Input Set : A:\txt.98,736.Seq.Lst.2nd.Rev.txt

Output Set: N:\CRF3\04182001\I218913B.raw

3 <110> APPLICANT: Hall, Roderick L
 4 Poll, Christopher T.
 5 Newton, Benjamin B.
 6 Taylor, William J.A.
 8 <120> TITLE OF INVENTION: A Method for Accelerating the Rate of Mucociliary Clearance
 W--> 9 <130> FILE REFERENCE: 98,736
 11 <140> CURRENT APPLICATION NUMBER: 09/218,913B
 12 <141> CURRENT FILING DATE: 1998-12-22
 14 <160> NUMBER OF SEQ ID NOS: 71
 16 <170> SOFTWARE: Microsoft Word 97
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 179
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapien
 23 <400> SEQUENCE: 1
 24 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
 25 1 5 10 15
 27 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
 28 20 25 30
 30 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
 31 35 40 45
 33 Asn Asn Tyr Leu Thr Lys Glu Cys Leu Lys Lys Cys Ala Thr Val
 34 50 55 60
 36 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
 37 65 70 75 80
 39 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
 40 85 90 95
 42 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
 43 100 105 110
 45 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
 46 115 120 125
 48 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
 49 130 135 140
 51 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
 52 145 150 155 160
 54 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
 55 165 170 175
 57 Ala Val Ser
 60 <210> SEQ ID NO: 2
 61 <211> LENGTH: 197
 62 <212> TYPE: PRT
 63 <213> ORGANISM: Homo sapien
 65 <220> FEATURE:
 66 <221> NAME/KEY: sig_peptide
 67 <222> LOCATION: 1..18
 69 <400> SEQUENCE: 2
 70 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val

ENTERED

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```

71 1          5          10          15
73 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
74          20          25          30
76 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
77          35          40          45
79 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
80          50          55          60
82 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
83 65          70          75          80
85 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
86          85          90          95
88 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
89          100          105          110
91 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
92          115          120          125
94 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
95          130          135          140
97 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
98 145          150          155          160
100 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
101          165          170          175
103 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
104          180          185          190
106 Ala Gly Ala Val Ser
107          195
109 <210> SEQ ID NO: 3
110 <211> LENGTH: 153
111 <212> TYPE: PRT
112 <213> ORGANISM: Homo sapien
114 <400> SEQUENCE: 3
115 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
116 1          5          10          15
118 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
119          20          25          30
121 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
122          35          40          45
124 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly
125          50          55          60
127 Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala
128 65          70          75          80
130 Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr
131          85          90          95
133 Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser
134          100          105          110
136 Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe
137          115          120          125
139 Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu
140          130          135          140
142 Ala Cys Met Leu Arg Cys Phe Arg Gln

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143 145                      150
145 <210> SEQ ID NO: 4
146 <211> LENGTH: 58
147 <212> TYPE: PRT
148 <213> ORGANISM: Homo sapien
150 <400> SEQUENCE: 4
151 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
152 1                      5                      10                      15
154 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
155                      20                      25                      30
157 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
158                      35                      40                      45
160 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
161 50                      55
163 <210> SEQ ID NO: 5
164 <211> LENGTH: 51
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapien
168 <400> SEQUENCE: 5
169 Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg
170 1                      5                      10                      15
172 Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
173                      20                      25                      30
175 Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu
176                      35                      40                      45
178 Lys Lys Cys
179 50
181 <210> SEQ ID NO: 6
182 <211> LENGTH: 58
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapien
186 <400> SEQUENCE: 6
187 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
188 1                      5                      10                      15
190 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
191                      20                      25                      30
193 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
194                      35                      40                      45
196 Glu Ala Cys Met Leu Arg Cys Phe Arg Gln
197 50                      55
199 <210> SEQ ID NO: 7
200 <211> LENGTH: 51
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapien
204 <400> SEQUENCE: 7
205 Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg
206 1                      5                      10                      15
208 Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly
209                      20                      25                      30

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211 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
 212 35 40 45
 214 Leu Arg Cys
 215 50

217 <210> SEQ ID NO: 8

218 <211> LENGTH: 92

219 <212> TYPE: PRT

220 <213> ORGANISM: Homo sapien

222 <400> SEQUENCE: 8

223 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val

224 1 5 10 15

226 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr

227 20 25 30

229 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser

230 35 40 45

232 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val

233 50 55 60

235 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp

236 65 70 75 80

238 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser

239 85 90

241 <210> SEQ ID NO: 9

242 <211> LENGTH: 708

243 <212> TYPE: DNA

244 <213> ORGANISM: Homo sapien

246 <220> FEATURE:

247 <221> NAME/KEY: misc_feature

248 <222> LOCATION: 679..708

249 <223> OTHER INFORMATION: /note= "n at positions 622, 679, 707 is any nucleic acid"

251 <400> SEQUENCE: 9

252 ggccgggtcg tttctcgctt ggctgggacg gctgctcctc tctgggggtcc tggcgccga 60

254 ccgagaacgc agcatccacg acttctgcct ggtgtcgaag gtggtgggca gatgccgggc 120

256 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg 180

258 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc 240

260 cactgtcaca gagaatgccca cgggtgacct ggccaccagc aggaatgcag cggattcctc 300

262 tgtcccaagt gctcccagaa ggcaggattc tgaagaccac tccagcgata tgttcaacta 360

264 tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcacact tcccacgctg 420

266 gtactttgac gtggagagga actcctgcaa taacttcac tatggaggct gccggggcaa 480

268 taagaacagc taccgctctg aggaggcctg catgctccgc tgcttccgac agcaggagaa 540

270 tcctccctcg ccccttggt caaagggtgt ggttctggcc ggggctgttt cgtgatgtg 600

272 ttgatccttt tcttggggag cttccatggt cttactgatt ccgggtggca aggaggaacc 660

274 aggagcgtgc cctgcggganc gtctggagct tcggagatga caagggt 708

276 <210> SEQ ID NO: 10

277 <211> LENGTH: 235

278 <212> TYPE: PRT

279 <213> ORGANISM: Homo sapien

281 <220> FEATURE:

282 <221> NAME/KEY: peptide

283 <222> LOCATION: 1..235

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284 <223> OTHER INFORMATION: /note= "Xaa at positions 198, 201, 226, and 233 are unknown
 285 amino acids"

287 <400> SEQUENCE: 10

288 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val

289 1 5 10 15

291 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser

292 20 25 30

294 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn

295 35 40 45

297 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly

298 50 55 60

300 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala

301 65 70 75 80

303 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala

304 85 90 95

306 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp

307 100 105 110

309 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala

310 115 120 125

312 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val

313 130 135 140

315 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn

316 145 150 155 160

318 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg

319 165 170 175

321 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu

322 180 185 190

W--> 324 Ala Gly Ala Val Ser Xaa Trp Cys Xaa Ser Phe Ser Trp Gly Ala Ser

325 195 200 205

327 Met Val Leu Leu Ile Pro Gly Gly Lys Glu Glu Pro Gly Ala Cys Pro

328 210 215 220

W--> 330 Ala Xaa Arg Leu Glu Leu Arg Arg Xaa Gln Gly

331 225 230 235

333 <210> SEQ ID NO: 11

334 <211> LENGTH: 179

335 <212> TYPE: PRT

336 <213> ORGANISM: Homo sapien

338 <220> FEATURE:

339 <221> NAME/KEY: peptide

340 <222> LOCATION: 1..170

341 <223> OTHER INFORMATION: /note= "Xaa at positions 8, 17, 19, 21-26, 40, 42, 45-47,

52, 64,

342 103, 112, 114, 116-121, 135, 137, 140-142, 147, and 159 is any

343 amino acid residue"

345 <400> SEQUENCE: 11

W--> 346 Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val

347 1 5 10 15

W--> 349 Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr

350 20 25 30

W--> 352 Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

file://

4/18/01

VERIFICATION SUMMARY

DATE: 04/18/2001

PATENT APPLICATION: US/09/218,913B

TIME: 10:40:12

Input Set : A:\txt.98,736.Seq.Lst.2nd.Rev.txt

Output Set: N:\CRF3\04182001\I218913B.raw

L:9 M:283 W: Missing Blank Line separator, <130> field identifier
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:427 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:598 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:992 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
L:1099 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
L:1206 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49